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**Prevalence of Human Papillomavirus (HPV) Infection from Cervical Swabs of Normal Women in Southern Selangor, Malaysia**A.R. Nurul Asyikin<sup>1,\*</sup>, R. Rozita<sup>2</sup>, C.K. Ng<sup>3</sup>, W.H. Wan Hamilton<sup>4</sup>, B.C. Tan<sup>5</sup>, M. Rusinahayati<sup>2</sup>, P.P. Chong<sup>1</sup><sup>1</sup> Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, UPM, Malaysia<sup>2</sup> Department of Obstetric and Gynecology, Faculty Of Medicine and Health Sciences, UPM, Malaysia<sup>3</sup> Department of Obstetric and Gynaecology, Kajang Hospital, Kajang, Malaysia<sup>4</sup> Department of Obstetric and Gynaecology, Serdang Hospital, Serdang, Malaysia<sup>5</sup> Britannia Women and Children Specialist Centre, Kajang, Malaysia

**Background:** Epidemiologic studies have clearly shown that infection with high-risk types of Human Papillomavirus (HPV), types 16 and 18 causes most cervical pre-neoplastic and neoplastic lesions. HPV 16 being common genotype found in general population but it still remains among the most prevalent individual type in cervical neoplasias. Since HPV testing is becoming a more useful and important tool for cervical cancer screening in the past few years, this study was conducted to detect the HPV infection rate among healthy women or non-cervical cancer patients and to identify the HPV genotype in HPV-positive samples.

**Methods:** In this study we performed nested PCR using primers targeting the L1 gene of HPV against DNA extracted from cervical swabs obtained from non-cervical cancer women or healthy women attending regular Pap Smear clinics. To ensure the validity of the results, the PCR experiments were repeated at least 3 times for each sample, and rigorous controls were incorporated. The HPV types from each PCR positive sample were identified by DNA sequencing. All patients who participated in this study were also given self-administered, standardized questionnaire regarding their lifestyle and sexual activity.

**Result:** 60 out of 70 (85.7%) samples were positive for HPV infections. The most common HPV DNA type found was type 16 (60%), followed by 18 (7.1%), 33 (2.8%), 58 (1.4%) and 87 (1.4%). HPV 16, 18 and 58 are high-risk types associated with development of cervical cancer; whereas HPV type 87 is thought to have low-to intermediate-risk.

**Conclusion:** Our findings indicate that there is a high prevalence of HPV infection among the women studied; whereby HPV type 16 was the most common genotype among the healthy female population in Southern Selangor. This underscores the importance of educating the public regarding the significance of regular Pap smear screening and the benefits of preventive immunization with HPV vaccine.

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**Respondent-Driven Sampling Technique to Study Prevalence of STI and HIV Among Female Sex Workers in Goa, India: Experiences from Field**S. Wayal<sup>1,\*</sup>, A. Copas<sup>2</sup>, F. Cowan<sup>2</sup>, V. Patel<sup>3</sup>, D. Mabey<sup>4</sup>, M. Shahmanesh<sup>5</sup><sup>1</sup> Positive People, Goa, India; and Brighton and Sussex Medical School, Brighton, United Kingdom<sup>2</sup> Centre for Sexual Health and HIV research, University College London, London, United Kingdom<sup>3</sup> Sangath, Goa, India; and London School of Hygiene and Tropical Medicine, London, United Kingdom<sup>4</sup> London School of Hygiene and Tropical Medicine, London, United Kingdom<sup>5</sup> Positive People, Goa, India; and Centre for Sexual Health and HIV research, University College London, London, United Kingdom

**Background:** Representative samples enables research to explore the patterns, risk factors and transmission dynamics of infectious diseases at a population level. Lack of population estimates of hidden groups like sex workers pose challenges to obtaining representative samples, thus compromising external validity. We aim to describe recruitment of female sex workers (FSWs) using respondent-driven sampling (RDS) to a HIV/STI epidemiology study conducted after the demolition of sex work (SW) area Baina in Goa, India. It was difficult to reach FSWs in the post-demolition period.

**Methods:** Ethnographic study of organisation of FSWs post-demolition (August-December 2004) led to recruitment of 59 'initial seeds' of different age, ethnicity and type of SW. They were paid \$2.50 for study participation and given three coupons to refer members from their social network, who in turn were also given three coupons to make referrals. Participants received \$1.25 for each successful referral they made. All participants also received free condoms, lubricants, treatment for STIs. Data was weighted to reduce potential recruitment bias (by social network size, age, ethnicity) using RDS Analysis Tool 5.4.0 (Cornell University, USA). Analyses were performed using Stata8, incorporating weights through survey analysis functions.

**Results:** 326 FSWs were recruited between November 2004-December 2005. Of the 59 initial seeds, 35 made referrals of which 57% made more than one referral. 5% of the FSWs who participated in the study refused to accept coupons to make referrals. RDS led to 6 recruitment waves. Majority had network size between 1 to 10. Substantial number of FSWs with no lifetime exposure to HIV prevention (61.3%) and 28% home-based FSWs throughout Goa were recruited indicating outreach of RDS to FSWs who might have been excluded in time-location or venue based sampling. Interpersonal dynamics and loose social networks among FSWs, and lack of trust meant more staff time per-recruited respondent.

**Conclusion:** RDS led to successful HIV/STI survey and could be used for implementing interventions among FSWs in Goa. However, extensive formative research, involvement of members proximate to FSWs, providing health related incentives played significant role in implementation of RDS